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Table S1. The list of identified *Bacteria* genera and their count in the shelf and deep-sea zones of the Black Sea

Таблица S1. Список идентифицированных родов бактерий и их количество в шельфовой и глубоководной зоне Чёрного моря

No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
1	*Thermomarinilinea*	151	162	165	393	342	206	1,419
2	*Syntrophaceticus*	20	20	56	236	112	46	490
3	*Romeriopsis*	51	25	38	31	69	143	357
4	*Anaerohalosphaera*	37	93	88	18	63	10	309
5	*Clostridium*	36	13	45	29	56	54	293
6	*Leptolinea*	128	30	32	59	38	4	291
7	*Thermanaerothrix*	135	52	47	11	10	27	282
8	*Koinonema*	6	19	31	54	107	25	242
9	*Anaerolinea*	59	47	38	43	32	16	235
10	*Leptothoe*	0	0	0	41	144	0	185
11	*Pelolinea*	51	31	17	31	47	6	183
12	*Quatrionicoccus*	12	8	10	16	25	111	182
13	*Litorilinea*	19	29	25	41	33	10	157
14	*Streptomyces*	20	28	7	4	28	42	129
15	*Ardenticatena*	29	8	18	67	7	0	129
16	*Caloribacterium*	0	0	0	7	29	84	120
17	*Dehalogenimonas*	5	13	19	10	62	0	109
18	*Haliangium*	15	20	14	3	11	43	106
19	*Herpetosiphon*	10	16	15	23	26	7	97
20	*Chloroherpeton*	4	0	6	71	12	0	93
21	*Rubrobacter*	20	3	10	36	12	5	86
22	*Sinocapsa*	5	6	15	27	20	9	82
23	*Desulforhopalus*	13	6	6	5	14	28	72
24	*Flexilinea*	11	7	11	21	18	4	72
25	*Anoxybacillus*	5	13	9	18	16	10	71
26	*Senegalia*	3	4	5	10	9	39	70
27	*Limihaloglobus*	5	23	15	8	14	4	69
28	*Sedimentisphaera*	7	21	5	12	22	0	67
29	*Brockia*	19	21	21	0	0	0	61
30	*Sandaracinus*	9	35	16	0	0	0	60
31	*Phycisphaera*	9	18	12	3	13	3	58
32	[*Eubacterium*]	7	13	9	7	13	8	57
33	*Euryhalocaulis*	0	0	0	0	11	46	57
34	*Ornatilinea*	8	8	5	26	7	0	54
35	*Planococcus*	10	11	8	9	13	3	54
36	*Panacagrimonas*	4	20	11	4	5	0	44

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No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
37	*Mycolicibacterium*	3	5	4	0	4	27	43
38	*Niallia*	5	0	9	11	10	7	42
39	*Syntrophorhabdus*	0	0	0	13	29	0	42
40	*Paenibacillus*	3	0	7	18	5	7	40
41	*Phaeochromatium*	6	4	5	12	6	6	39
42	*Desulfofrigus*	3	4	7	14	8	3	39
43	*Gansulinema*	0	0	5	18	16	0	39
44	*Kovacikia*	4	0	5	0	10	19	38
45	*Thermogemmatispora*	25	5	4	3	0	0	37
46	*Vulcanimicrobium*	0	0	4	0	3	27	34
47	*Bacillus*	3	4	0	9	5	12	33
48	*Chlorobaculum*	0	9	24	0	0	0	33
49	*Halobacillus*	7	8	4	3	5	5	32
50	*Thermodesulfovibrio*	0	3	10	4	3	12	32
51	*Kushneria*	10	9	6	0	7	0	32
52	*Ilumatobacter*	6	6	3	7	4	6	32
53	*Dehalococcoides*	7	5	0	8	7	4	31
54	*Euzebya*	3	0	5	5	18	0	31
55	*Acidicapsa*	0	0	0	6	25	0	31
56	*Caulobacter*	0	0	3	3	25	0	31
57	*Thermoflavimicrobium*	6	0	11	3	6	3	29
58	*Halomonas*	4	3	0	4	6	12	29
59	*Sinomonas*	4	0	6	10	3	6	29
60	*Thermaerobacter*	0	4	6	5	8	6	29
61	*Algorimarina*	9	10	5	0	4	0	28
62	*Calorithrix*	6	3	4	6	9	0	28
63	*Oxobacter*	3	4	7	14	0	0	28
64	*Egbenema*	0	3	3	6	0	15	27
65	*Pelosinus*	0	19	5	0	3	0	27
66	*Tepidanaerobacter*	3	0	8	6	10	0	27
67	*Thermobaculum*	12	4	0	0	0	11	27
68	*Cyanothece*	7	0	0	3	15	0	25
69	*Corynebacterium*	9	3	0	0	4	5	21
70	*Enterococcus*	9	0	3	3	3	4	22
71	*Phototrophicus*	9	4	4	0	0	3	20
72	*Terrimesophilobacter*	9	0	0	0	0	0	9
73	*Nitrosococcus*	8	3	0	0	0	0	11
74	*Bacterioplanoides*	7	0	0	0	5	0	12
75	*Bellilinea*	7	0	0	0	0	0	7
76	*Desulfatiglans*	7	6	3	0	0	0	16
77	*Fictibacillus*	7	0	0	0	8	8	23
78	*Urbifossiella*	7	3	0	0	0	0	10
79	*Dokdonella*	6	4	3	0	0	5	18
80	*Maridesulfovibrio*	6	5	0	3	4	5	23
81	*Succiniclasticum*	6	8	0	0	0	0	14
82	*Desulfacinum*	5	3	0	0	3	0	11
83	*Desulfofustis*	5	0	0	0	0	3	8
84	*Desulforapulum*	5	0	0	0	0	0	5

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No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
85	*Geotalea*	5	4	3	0	0	0	12
86	*Megasphaera*	5	8	3	4	4	0	24
87	*Paraburkholderia*	5	6	15	0	0	0	26
88	*Turneriella*	5	0	4	3	0	0	12
89	*Woeseia*	5	0	6	0	0	0	11
90	*Anaerotignum*	4	0	0	0	0	0	4
91	*Arboricoccus*	4	3	0	0	0	0	7
92	*Caldanaerobius*	4	3	0	0	0	0	7
93	*Chitinispirillum*	4	0	5	4	3	0	16
94	*Desulfallas*	4	7	0	0	0	0	11
95	*Desulfobacca*	4	7	3	3	0	0	17
96	*Erysipelothrix*	4	3	0	0	0	0	7
97	*Gloeomargarita*	4	5	0	0	10	0	19
98	*Ignavibacterium*	4	0	0	0	0	0	4
99	*Saccharomonospora*	4	0	5	0	8	0	17
100	*Simkania*	4	6	0	0	0	0	10
101	*Swaminathania*	4	0	0	0	0	0	4
102	*Tamilnaduibacter*	4	0	0	0	0	0	4
103	*Thermoanaerobaculum*	4	0	0	0	0	0	4
104	*Thermoflexus*	4	0	0	7	4	3	18
105	*Thioalkalivibrio*	8	4	0	3	3	4	22
106	*Acinetobacter*	3	0	0	0	0	0	3
107	*Aggregatilinea*	3	3	0	0	3	0	9
108	*Atlanticothrix*	3	0	0	0	5	5	13
109	*Brevibacillus*	3	0	0	0	0	3	6
110	*Butyribacter*	3	0	0	3	0	0	6
111	*Caballeronia*	3	3	0	0	0	0	6
112	*Caldanaerobacter*	3	4	0	4	0	0	11
113	*Carboxylicivirga*	3	0	0	0	0	0	3
114	*Constrictibacter*	3	0	0	0	0	0	3
115	*Coxiella*	3	6	6	0	0	0	15
116	*Dankookia*	3	0	0	0	0	0	3
117	*Desulfobacterium*	3	0	3	0	0	0	6
118	*Desulfocella*	3	0	0	0	0	0	3
119	*Desulforegula*	3	3	0	0	0	0	6
120	*Desulfotalea*	3	0	0	0	0	0	3
121	*Desulfurella*	3	0	0	0	3	0	6
122	*Desulfuromonas*	3	7	0	0	0	0	10
123	*Dolosigranulum*	3	0	0	0	0	0	3
124	*Ezakiella*	3	0	0	0	0	0	3
125	*Fervidobacterium*	3	5	0	0	6	0	14
126	*Fusibacter*	3	0	0	0	0	0	3
127	*Halorhodospira*	3	0	0	0	0	0	3
128	*Halothermothrix*	3	0	0	0	0	0	3
129	*Humidesulfovibrio*	3	0	0	0	3	3	9
130	*Klebsiella*	3	0	0	0	0	0	3
131	*Leptospirillum*	3	0	0	0	0	0	3
132	*Ligaoa*	3	0	0	3	0	0	6

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No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
133	*Luteibacter*	3	0	0	0	0	0	3
134	*Marimicrobium*	3	0	0	0	0	0	3
135	*Mucisphaera*	3	0	0	0	3	0	6
136	*Oligosphaera*	3	3	5	4	3	0	18
137	*Paenibacillus*	3	0	0	0	0	0	3
138	*Paraclostridium*	3	0	0	0	5	0	8
139	*Parasynechococcus*	3	0	0	0	0	0	3
140	*Pediococcus*	3	0	0	4	4	0	11
141	*Pseudarthrobacter*	3	0	0	0	0	8	11
142	*Pseudonocardia*	3	0	0	0	0	0	3
143	*Roseobacter*	3	0	0	0	0	0	3
144	*Rubneribacter*	3	0	0	0	0	0	3
145	*Salibacterium*	3	0	0	0	0	0	3
146	*Sedimentibacter*	3	3	0	0	0	0	6
147	*Sinobacterium*	3	0	0	0	0	0	3
148	*Solimonas*	3	0	0	0	4	0	7
149	*Spirillospora*	3	5	6	5	5	0	24
150	*Syntrophus*	3	0	8	0	0	0	11
151	*Tepidisphaera*	3	0	0	0	0	0	3
152	*Thermodesulforhabdus*	3	8	0	0	0	0	11
153	*Thermostaphylospora*	3	0	0	0	0	0	3
154	*Thermostilla*	3	0	0	0	0	0	3
155	*Thiocystis*	3	0	0	0	6	4	13
156	*Thiolapillus*	3	0	4	0	7	10	24
157	*Tichowtungia*	3	4	0	0	0	0	7
158	*Ursidibacter*	3	0	0	0	0	0	3
159	*Abiotrophia*	0	0	0	0	7	0	7
160	*Acanthopleuribacter*	0	0	10	0	0	0	10
161	*Acetatifactor*	0	3	0	0	0	0	3
162	*Acetivibrio*	0	0	0	7	0	0	7
163	*Acidimicrobium*	0	0	0	3	0	6	9
164	*Actinocorallia*	0	0	0	0	0	4	4
165	*Actinomadura*	0	8	0	4	3	5	20
166	*Actinoplanes*	0	5	0	0	0	5	10
167	*Actinopolyspora*	0	3	0	0	0	0	3
168	*Actinorectispora*	0	0	3	3	4	3	13
169	*Aerococcus*	0	0	0	0	3	0	3
170	*Agromyces*	0	0	0	0	3	5	8
171	*Albibacter*	0	0	4	0	3	0	7
172	*Altererythrobacter*	0	0	0	0	4	0	4
173	*Aminicella*	0	0	0	0	3	0	3
174	*Anaerobranca*	0	0	3	0	0	9	12
175	*Anaerococcus*	0	0	0	3	20	0	23
176	*Anaerocolumna*	0	0	3	0	0	0	3
177	*Anaeromonas*	0	0	0	0	0	4	4
178	*Aquihabitans*	0	0	3	0	0	0	3
179	*Aquimarina*	0	3	0	0	0	0	3
180	*Arenimonas*	0	4	3	0	0	0	7

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No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
181	*Asticcacaulis*	0	0	0	0	5	0	5
182	*Atopobium*	0	0	0	0	0	3	3
183	*Atribacter*	0	0	4	0	0	5	9
184	*Aureimonas*	0	0	0	0	0	3	3
185	*Azospirillum*	0	5	0	0	0	0	5
186	*Bifidobacterium*	0	3	4	0	0	0	7
187	*Billgrantia*	0	3	0	0	3	0	6
188	*Blautia*	0	6	4	0	0	0	10
189	*Botrimarina*	0	0	0	0	3	0	3
190	*Bounagaea*	0	8	4	4	0	0	16
191	*Brevundimonas*	0	3	0	0	0	0	3
192	*Burkholderia*	0	0	0	0	3	0	3
193	*Candidatus Protochlamydia*	0	0	3	0	0	0	3
194	*Chloracidobacterium*	0	15	4	0	0	0	19
195	*Chroococcidiopsis*	0	0	0	0	5	0	5
196	*Chryseosolibacter*	0	0	0	0	5	0	5
197	*Chthonomonas*	0	0	0	0	0	3	3
198	*Cohnella*	0	0	0	3	3	0	6
199	*Corallococcus*	0	0	3	0	0	0	3
200	*Crassaminicella*	0	3	0	0	4	0	7
201	*Dapisostemon*	0	0	3	11	10	0	24
202	*Defluviitalea*	0	4	3	14	0	0	21
203	*Deinococcus*	0	0	0	23	0	0	23
204	*Desulfarculus*	0	0	0	0	4	0	4
205	*Desulfatirhabdium*	0	4	4	0	0	0	8
206	*Desulfobulbus*	0	3	0	0	0	0	3
207	*Desulfohalophilus*	0	11	0	0	0	0	11
208	*Desulfolucanica*	0	4	0	0	0	0	4
209	*Desulfomonile*	0	3	3	0	0	0	6
210	*Desulfonatronospira*	0	0	3	3	4	0	10
211	*Desulforamulus*	0	0	0	3	6	0	9
212	*Desulfosalsimonas*	0	0	3	3	0	0	6
213	*Desulfovirgula*	0	0	0	0	3	0	3
214	*Desulfuromusa*	0	3	0	0	0	0	3
215	*Emergencia*	0	0	0	0	4	0	4
216	*Enterobacter*	0	0	3	0	3	0	6
217	*Ercella*	0	0	0	5	0	0	5
218	*Exiguobacterium*	0	0	0	9	0	0	9
219	*Exilispira*	0	3	0	0	5	0	8
220	*Feifania*	0	0	0	4	0	0	4
221	*Fibrobacter*	0	0	0	0	4	0	4
222	*Filomicrobium*	0	4	0	0	0	0	4
223	*Fimbriimonas*	0	0	5	0	0	0	5
224	*Flexistipes*	0	0	4	0	0	0	4
225	*Fontisphaera*	0	0	0	0	0	3	3
226	*Frisingicoccus*	0	0	0	0	0	5	5
227	*Gelria*	0	0	4	0	14	0	18
228	*Geobacillus*	0	0	0	3	0	0	3

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No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
229	*Gilvimarinus*	0	0	3	0	0	0	3
230	*Gleimia*	0	0	0	0	6	0	6
231	*Gottfriedia*	0	0	5	3	0	0	8
232	*Gracilibacillus*	0	0	0	4	0	0	4
233	*Haemophilus*	0	0	0	0	3	0	3
234	*Halanaerobacter*	0	0	0	6	9	0	15
235	*Halarsenatibacter*	0	6	5	4	0	4	19
236	*Haloactinomyces*	0	0	0	0	3	8	11
237	*Heliobacterium*	0	0	0	0	3	0	3
238	*Hillbrichtia*	0	0	0	5	10	0	15
239	*Holospora*	0	0	0	0	4	0	4
240	*Hydrotalea*	0	3	0	0	0	0	3
241	*Iamia*	0	3	3	0	3	0	9
242	*Immundisolibacter*	0	6	0	0	0	0	6
243	*Jeotgalicoccus*	0	3	0	3	0	0	6
244	*Kiritimatiella*	0	6	0	0	7	0	13
245	*Kitasatospora*	0	0	0	0	0	5	5
246	*Labilithrix*	0	0	0	6	7	0	13
247	*Leptonema*	0	0	3	0	0	0	3
248	*Levilinea*	0	0	6	4	0	0	10
249	*Lichenifustis*	0	0	0	0	3	0	3
250	*Limisphaera*	0	3	0	0	0	0	3
251	*Limosilactobacillus*	0	0	0	0	5	0	5
252	*Lyngbya*	0	0	0	0	5	4	9
253	*Lysinibacillus*	0	0	5	4	0	0	9
254	*Macrochaete*	0	0	0	3	3	0	6
255	*Mahella*	0	0	0	4	3	6	13
256	*Malacoplasma*	0	3	0	0	0	0	3
257	*Mariniflexile*	0	7	0	0	0	0	7
258	*Marinimicrobium*	0	0	0	0	9	0	9
259	*Marininema*	0	3	5	7	0	0	15
260	*Megalodesulfovibrio*	0	0	0	0	6	0	6
261	*Meiothermus*	0	0	0	3	5	0	8
262	*Meniscus*	0	0	0	0	4	0	4
263	*Metamycoplasma*	0	0	0	0	0	4	4
264	*Methylothermalis*	0	0	0	0	0	7	7
265	*Modestobacter*	0	0	0	3	0	0	3
266	*Moorella*	0	0	0	4	0	0	4
267	*Moraxella*	0	0	0	0	3	0	3
268	*Mycobacterium*	0	0	0	0	0	5	5
269	*Neochlamydia*	0	0	0	0	6	6	12
270	*Nitriliruptor*	0	0	0	0	0	3	3
271	*Nitrosomonas*	0	0	5	3	0	0	8
272	*Nitrosophilus*	0	0	0	0	8	0	8
273	*Nitrosospira*	0	0	4	0	0	0	4
274	*Nocardiopsis*	0	0	0	0	0	3	3
275	*Novosphingobium*	0	3	0	0	7	0	10
276	*Oceanirhabdus*	0	0	0	0	6	0	6

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No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
277	*Olegusella massiliensis*	0	0	0	0	8	0	8
278	*Oscillatoria*	0	0	0	3	6	4	13
279	*Paenibacillus*	0	0	0	0	6	0	6
280	*Pannus*	0	0	4	0	0	5	9
281	*Paracidovorax*	0	0	0	0	4	0	4
282	*Paraclostridium*	0	5	0	0	0	0	5
283	*Paracoccus*	0	4	0	0	0	0	4
284	*Paractinoplanes*	0	0	4	0	12	3	19
285	*Paramaledivibacter*	0	0	0	0	3	0	3
286	*Pararhodospirillum*	0	0	3	8	4	0	15
287	*Parasediminibacterium*	0	0	3	0	0	0	3
288	*Pelagerythrobacter*	0	0	0	0	3	0	3
289	*Peptidiphaga*	0	3	0	0	0	0	3
290	*Peptostreptococcus*	0	0	3	0	0	3	6
291	*Phenylobacterium*	0	0	0	0	5	0	5
292	*Phormidium irriguum*	0	0	0	0	9	0	9
293	*Phyllonema*	0	0	6	0	0	0	6
294	*Priestia*	0	0	0	0	4	0	4
295	*Pseudoflavonifractor*	0	0	0	3	0	0	3
296	*Pseudomonas*	0	0	0	4	0	0	4
297	*Puteibacter*	0	0	0	4	6	0	10
298	*Quadrisphaera*	0	0	4	0	0	0	4
299	*Rahnella*	0	0	6	0	3	0	9
300	*Rhodoplanes*	0	4	0	0	0	0	4
301	*Rickettsia*	0	3	0	0	0	0	3
302	*Roseospirillum*	0	0	4	0	4	4	12
303	*Saccharopolyspora*	0	0	0	3	0	0	3
304	*Salinicoccus*	0	0	3	0	0	0	3
305	*Salinivibrio*	0	0	4	0	8	0	12
306	*Sediminihaliea*	0	6	4	4	0	0	14
307	*Segniliparus*	0	0	0	3	6	0	9
308	*Shigella*	0	0	0	0	3	0	3
309	*Sinobaca*	0	0	3	0	3	0	6
310	*Solirubrobacter*	0	0	0	15	0	0	15
311	*Sphingobium*	0	0	0	0	4	0	4
312	*Sphingomonas*	0	0	0	0	11	0	11
313	*Spirillum*	0	0	0	3	3	0	6
314	*Spirochaeta*	0	0	0	3	4	0	7
315	*Spirulina*	0	0	0	0	0	3	3
316	*Sporanaerobium*	0	0	3	0	0	0	3
317	*Sporotomaculum*	0	0	5	0	0	17	22
318	*Stackebrandtia*	0	0	0	0	0	3	3
319	*Syntrophothermus*	0	0	3	3	0	0	6
320	*Tepidicaulis*	0	0	4	0	0	0	4
321	*Thermacetogenium*	0	0	13	0	0	0	13
322	*Thermobifida*	0	4	3	0	3	0	10
323	*Thermocaproicibacter*	0	0	3	0	0	3	6
324	*Thermochromatium*	0	0	0	10	0	0	10

Contunued on the next page…

No.	Genus	Shelf zone			Deep-sea zone			Total
		bar2	bar3	bar4	bar5	bar6	bar7	
325	*Thermogutta*	0	0	0	0	3	0	3
326	*Thermohalobacter*	0	0	0	3	3	0	6
327	*Thermomonospora*	0	0	3	0	13	6	22
328	*Thermosulfurimonas*	0	6	0	0	0	0	6
329	*Thiobacillus*	0	0	0	0	4	0	4
330	*Thiorhodococcus*	0	0	0	3	0	0	3
331	*Treponema*	0	0	0	0	3	0	3
332	*Venetifunis*	0	0	0	3	5	0	8
333	*Vulcanithermus*	0	0	0	4	5	0	9
334	*Wilmottia*	0	0	0	3	0	0	3
335	*Winkia*	0	0	0	0	0	3	3

Table S2. The presence of *Bacteria* families in the shelf and deep-sea zones of the Black Sea

Таблица S2. Наличие семейств бактерий в шельфовой и глубоководной зоне Чёрного моря

Phylum	Family	Number of strains	Shelf zone	Deep-sea zone
Chloroflexota	*Anaerolineaceae*	10	10	9
	Dehalococcoidaceae	3	+	+
	Ardenticatenaceae	1	+	+
	Thermogemmatisporaceae	1	+	+
	Caldilineaceae	1	+	+
	Chloroflexota incertae sedis	1	+	+
	Herpetosiphonaceae	1	+	+
	Phototrophicaceae	1	+	+
	Thermoflexaceae	1	+	+
	Aggregatilineaceae	1	+	+
Cyanobacteriota	*Leptolyngbyaceae*	2	+	+
	Cyanothecaceae	2	1	2
	Oscillatoriaceae	5	4	5
	Oscillatoriales incertae sedis	1	–	+
	Oculatellaceae	2	+	+
	Sinocapsaceae	1	+	+
	Nostocaceae	1	+	+
	Gloeomargaritaceae	1	+	+
	Prochlorococcaceae	1	+	–
	Dapisostemonaceae	1	+	+
	Chroococcidiopsidaceae	1	–	+
	Cymatolegaceae	1	–	+
	Calotrichaceae	1	–	+
	Microcystaceae	1	+	+
	Rivulariaceae	1	+	–
	Spirulinaceae	1	–	+
	Trichocoleusaceae	1	–	+
	Wilmottiaceae	1	–	+

Continued on the next page…

Phylum	Family	Number of strains	Shelf zone	Deep-sea zone
Planctomycetota	*Anaerohalosphaeraceae*	1	+	+
	Phycisphaeraceae	1	+	+
	Gemmataceae	1	+	–
	Sedimentisphaeraceae	3	+	+
	Thermoguttaceae	2	1	1
	Phycisphaeraceae	1	+	+
	Tepidisphaeraceae	1	+	–
	Lacipirellulaceae	1	–	+
Bacillota	*Clostridiaceae*	12	6	12
	Thermoanaerobacterales Family III	1	+	+
	Thermoanaerobacterales Family IV	1	–	+
	Bacillales Family X. incertae sedis	1	+	–
	Bacillales Family XII. incertae sedis	1	–	+
	Planococcaceae	1	+	+
	Enterococcaceae	2	1	1
	Bacillaceae	15	8	14
	Acidaminococcaceae	1	+	–
	Thermoactinomycetaceae	2	+	+
	Veillonellaceae	2	2	1
	Eubacteriales Family XIII. incertae sedis	3	2	2
	Eubacteriales Family XII. incertae sedis	1	+	–
	Anaerotignaceae	1	+	–
	Thermoanaerobacteraceae	6	4	4
	Desulfallaceae	2	2	1
	Erysipelotrichaceae	2	+	–
	Paenibacillaceae	5	3	4
	Lachnospiraceae	7	5	3
	Lactobacillaceae	2	1	2
	Carnobacteriaceae	1	+	–
	Tissierellia incertae sedis	2	+	–
	Halothermotrichaceae	1	+	–
	Oscillospiraceae	5	2	5
	Peptostreptococcaceae	3	3	2
	Aerococcaceae	2	–	+
	Anaerovoracaceae	2	–	+
	Proteinivoraceae	1	+	+
	Peptoniphilaceae	1	–	+
	Defluviitaleaceae	1	+	+
	Peptococcaceae	2	1	1
	Tepidanaerobacteraceae	1	+	+
	Eubacteriaceae	2	1	1
	Feifaniaceae	1	–	+
	Halobacteroidaceae	1	–	+
	Halarsenatibacteraceae	1	+	+
	Heliobacteriaceae	1	–	+
	Staphylococcaceae	2	2	1
	Moorellaceae	1	–	+
	Caminicellaceae	1	–	+

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Phylum	Family	Number of strains	Shelf zone	Deep-sea zone
	Sporomusaceae	1	+	+
	Sporolactobacillaceae	1	+	+
	Syntrophomonadaceae	1	+	+
	Clostridiales Family XVII. incertae sedis	1	+	+
	Thermohalobacteraceae	1	–	+
Myxococcota	*Kofleriaceae*	1	+	+
	Sandaracinaceae	1	+	–
	Myxococcaceae	1	+	–
	Labilitrichaceae	1	–	+
Thermodesulfobacteriota	*Desulfocapsaceae*	3	3	2
	Desulfobacteraceae	4	4	2
	Desulfovibrionaceae	3	2	3
	Desulfatiglandaceae	1	+	–
	Syntrophobacteraceae	2	1	1
	Geobacteraceae	1	+	–
	Desulfobaccaceae	1	+	+
	Desulfobacteriaceae	1	+	–
	Desulforegulaceae	1	+	–
	Desulfuromonadaceae	1	+	–
	Syntrophaceae	1	+	–
	Thermodesulforhabdaceae	1	+	+
	Desulfarculaceae	1	–	+
	Desulfatirhabdiaceae	1	+	–
	Desulfobulbaceae	1	+	–
	Desulfohalobiaceae	1	+	–
	Desulfomonilaceae	1	+	–
	Desulfonatronovibrionaceae	1	+	+
	Desulfosalsimonadaceae	1	+	+
	Geopsychrobacteraceae	1	+	–
	Syntrophorhabdaceae	1	–	+
	Thermodesulfobacteriaceae	1	+	–
Pseudomonadota	*Ectothiorhodospiraceae*	3	3	1
	Azonexaceae	1	+	+
	Halomonadaceae	4	3	4
	Chromatiaceae	5	3	4
	Oceanospirillaceae	1	+	–
	Rhodanobacteraceae	2	2	1
	Burkholderiaceae	5	4	1
	Woeseiaceae	1	+	–
	Geminicoccaceae	1	+	–
	Nevskiaceae	2	+	+
	Acetobacteraceae	2	+	–
	Marinobacteraceae	1	+	–
	Moraxellaceae	2	1	1
	Stellaceae	1	+	–
	Coxiellaceae	1	+	–
	Enterobacteriaceae	3	2	2
	Halieaceae	2	2	1

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Phylum	Family	Number of strains	Shelf zone	Deep-sea zone
	Roseobacteraceae	1	+	–
	Spongiibacteraceae	1	+	–
	Sedimenticolaceae	1	+	+
Pseudomonadota	*Pasteurellaceae*	2	1	1
	Methylopilaceae	2	1	1
	Erythrobacteraceae	2	–	+
	Lysobacteraceae	1	+	–
	Caulobacteraceae	4	2	3
	Aurantimonadaceae	1	–	+
	Azospirillaceae	1	+	–
	Maricaulaceae	1	–	+
	Hyphomicrobiaceae	3	2	1
	Cellvibrionaceae	2	1	1
	Holosporaceae	1	–	+
	Immundisolibacteraceae	1	+	–
	Lichenihabitantaceae	1	–	+
	Nitrosomonadaceae	3	2	1
	Sphingomonadaceae	4	1	4
	Comamonadaceae	1	–	+
	Paracoccaceae	1	+	–
	Rhodospirillaceae	3	1	3
	Pseudomonadaceae	2	1	1
	Yersiniaceae	1	+	+
	Rickettsiaceae	1	+	–
	Vibrionaceae	1	+	+
	Spirillaceae	1	–	+
	Parvibaculaceae	1	+	–
	Thiobacillaceae	1	–	+
Actinomycetota	*Rubrobacteraceae*	3	3	2
	Corynebacteriaceae	3	2	1
	Microbacteriaceae	2	1	1
	Ilumatobacteraceae	2	2	1
	Acidimicrobiaceae	1	–	+
	Streptomycetaceae	14	8	10
	Pseudonocardiaceae	4	3	3
	Micrococcaceae	3	2	2
	Euzebyaceae	1	+	+
	Mycobacteriaceae	4	1	4
	Eggerthellaceae	1	+	–
	Thermomonosporaceae	7	4	6
	Micromonosporaceae	2	+	+
	Actinopolysporaceae	2	1	1
	Iamiaceae	2	2	1
	Atopobiaceae	1	–	+
	Bifidobacteriaceae	2	+	–
	Actinomycetes incertae sedis	1	+	+
	Actinomycetaceae	3	1	2
	Geodermatophilaceae	1	–	+

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Phylum	Family	Number of strains	Shelf zone	Deep-sea zone
	Nitriliruptoraceae	1	–	+
	Nocardiopsaceae	2	1	2
	Coriobacteriaceae	1	–	+
	Kineosporiaceae	1	+	–
	Segniliparaceae	1	–	+
	Solirubrobacteraceae	1	–	+
	Glycomycetaceae	1	–	+
Calditrichota	*s__Calorithrix*	1	+	+
Spirochaetota	*Leptospiraceae*	2	2	1
	Spirochaetales incertae sedis	1	+	+
	Spirochaetaceae	1	–	+
	Treponemataceae	1	–	+
Fibrobacterota	*Chitinispirillaceae*	1	+	+
	Fibrobacteraceae	1	–	+
Chlorobiota	*Chloroherpetonaceae*	1	+	+
	Chlorobiaceae	1	+	–
Ignavibacteriota	*Ignavibacteriaceae*	1	+	–
Chlamydiota	*Simkaniaceae*	1	+	–
	Parachlamydiaceae	2	+	+
Acidobacteriota	*Thermoanaerobaculaceae*	1	+	–
	Acanthopleuribacteraceae	1	+	–
	Acidobacteriaceae	1	–	+
	Chloracidobacterium	1	+	–
Bacteroidota	*Marinilabiliaceae*	1	+	–
	Flavobacteriaceae	2	+	–
	Chryseotaleaceae	1	–	+
	Prolixibacteraceae	2	–	+
	Chitinophagaceae	2	+	–
Campylobacterota	*Desulfurellaceae*	1	+	+
	Nitratiruptoraceae	1	–	+
Thermotogota	*Fervidobacteriaceae*	1	+	+
Nitrospirota	*Nitrospiraceae*	1	+	–
	Thermodesulfovibrionaceae	2	2	1
Lentisphaerota	*Oligosphaeraceae*	1	+	+
Kiritimatiellota	*Tichowtungiaceae*	1	+	–
	Kiritimatiellaceae	1	+	+
Deinococcota	*Thermaceae*	2	–	+
	Deinococcaceae	1	–	+
Armatimonadota	*Fimbriimonadaceae*	1	+	–
	Chthonomonadaceae	1	–	+
Deferribacterota	*Flexistipitaceae*	1	+	–
Verrucomicrobiota	*Fontisphaeraceae*	1	–	+
	Limisphaeraceae	1	+	–
Mycoplasmatota	*Mycoplasmoidaceae*	1	+	–
	Metamycoplasmataceae	1	–	+
Vulcanimicrobiota	*Vulcanimicrobiaceae*	1	+	+
Atribacterota	*Atribacteraceae*	1	+	+

Table S3. The count of representatives of the most abundant *Bacteria* genera in two zones of the Black Sea

Таблица S3. Количество представителей наиболее распространённых родов бактерий в двух зонах Чёрного моря

No.	Phylum	Class	Genus	Shelf zone			Deep-sea zone		
				bar2	bar3	bar4	bar5	bar6	bar7
1	*Ch*	*Anaerolineae*	*Thermomarinilinea*	151	162	165	393	342	206
2			*Leptolinea*	128	30	32	59	38	4
3			*Thermanaerothrix*	135	52	47	11	10	27
4			*Anaerolinea*	59	47	38	43	32	16
5			*Pelolinea*	51	31	17	31	47	6
6		*Caldilineae*	*Litorilinea*	19	29	25	41	33	10
7		*Ardenticatenia*	*Ardenticatena*	29	8	18	67	7	0
8	*Cy*	*Cyanophyceae*	*Romeriopsis*	51	25	38	31	69	143
9			*Koinonema*	6	19	31	54	107	25
10			*Leptothoe*	0	0	0	41	144	0
11	*Ba*	*Clostridia*	*Syntrophaceticus*	20	20	56	236	112	46
12			*Clostridium*	36	13	45	29	56	54
13	*Pl*	*Phycisphaerae*	*Anaerohalosphaera*	37	93	88	18	63	10
14	*Ps*	*Betaproteobacteria*	*Quatrionicoccus*	12	8	10	16	25	111
15	*Ac*	*Actinomycetes*	*Streptomyces*	20	28	7	4	28	42

Note: *Ch*, *Chloroflexota*; *Cy*, *Cyanobacteriota*; *Ba*, *Bacillota*; *Pl*, *Planctomycetota*; *Ps*, *Pseudomonadota*; *Ac*, *Actinomycetota*.

Примечание: *Ch* — *Chloroflexota*; *Cy* — *Cyanobacteriota*; *Ba* — *Bacillota*; *Pl* — *Planctomycetota*; *Ps* — *Pseudomonadota*; *Ac* — *Actinomycetota*.

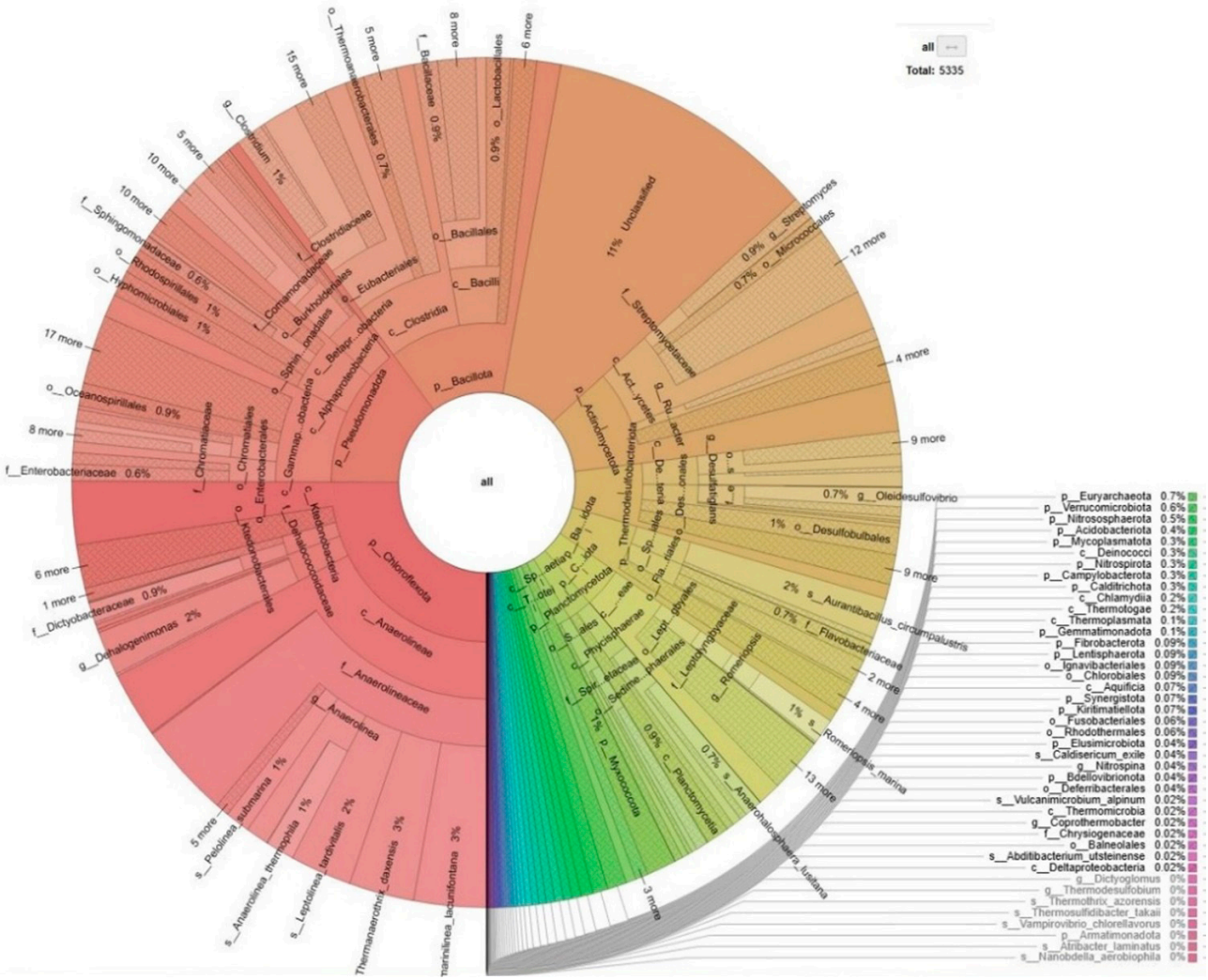

Fig. S1a. The Black Sea bacterial communities represented by dominant operational taxonomic units (OTUs) at different levels from samples of bottom sediments; the sample bar2 (st. 2, depth of 49 m, layer of bottom sediments of 20–25 cm)

Рис. S1a. Бактериальные сообщества Чёрного моря, представленные доминирующими операционными таксономическими единицами (OTU) на разных уровнях в пробах донных отложений; проба bar2 (ст. 2, глубина 49 м, слой донных отложений 20–25 см)

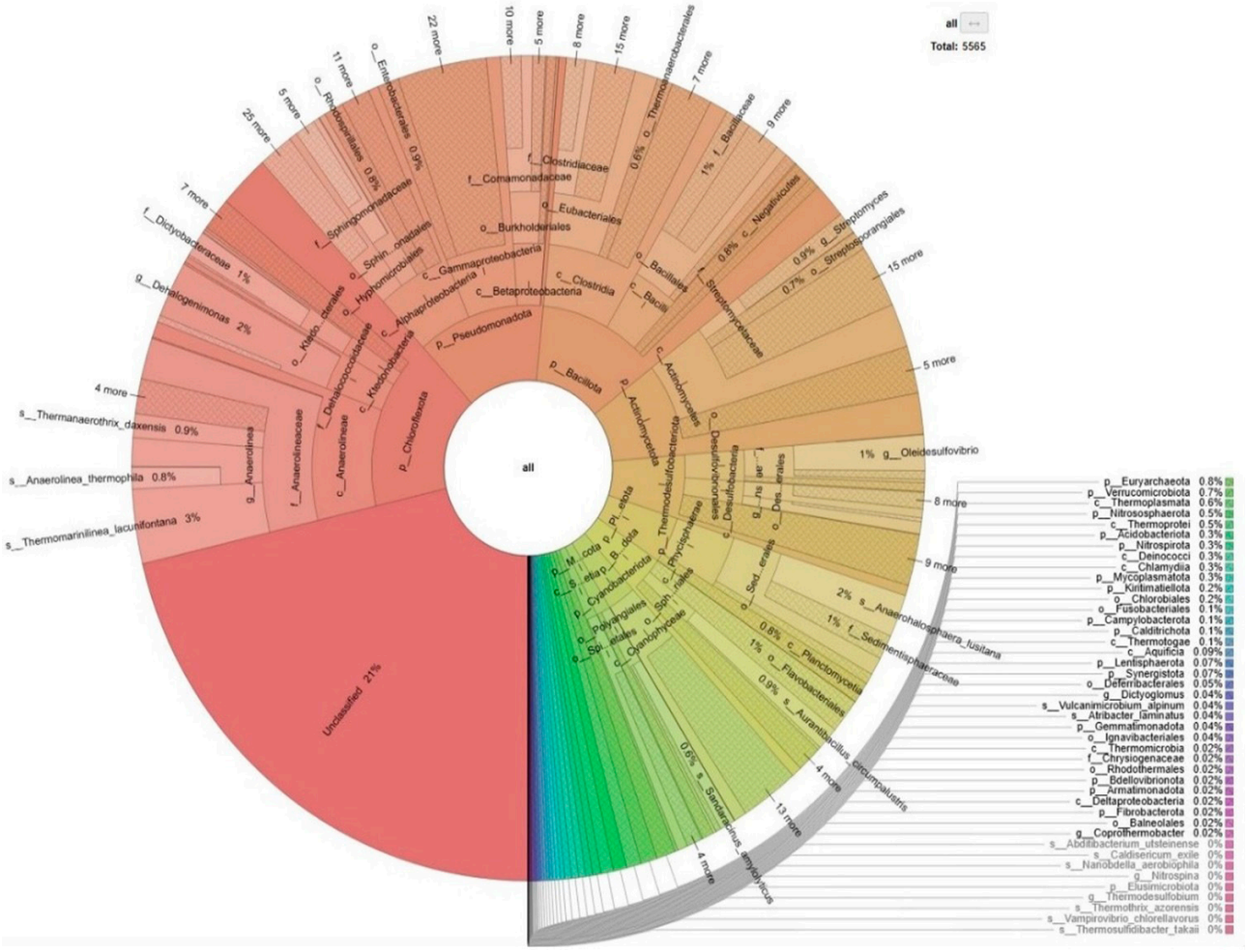

Fig. S1b. The Black Sea bacterial communities represented by dominant OTUs at different levels from samples of bottom sediments; the sample bar3 (st. 2, depth of 49 m, layer of bottom sediments of 40–45 cm)

Рис. S1b. Бактериальные сообщества Чёрного моря, представленные доминирующими OTU на разных уровнях в пробах донных отложений; проба bar3 (ст. 2, глубина 49 м, слой донных отложений 40–45 см)

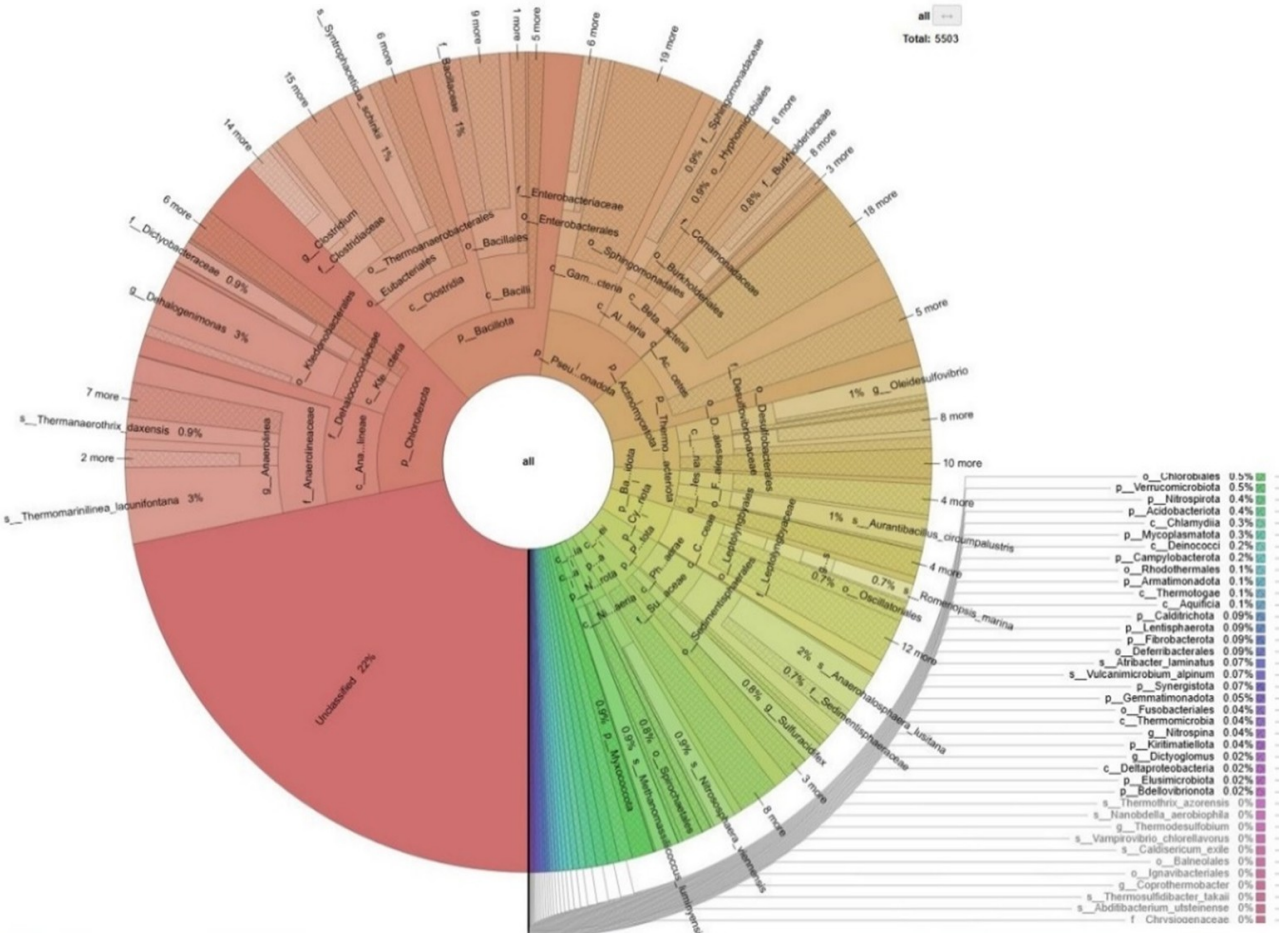

Fig. S1c. The Black Sea bacterial communities represented by dominant OTUs at different levels from samples of bottom sediments; the sample bar4 (st. 2, depth of 49 m, layer of bottom sediments of 65–70 cm)

Рис. S1c. Бактериальные сообщества Чёрного моря, представленные доминирующими OTU на разных уровнях в пробах донных отложений; проба bar4 (ст. 2, глубина 49 м, слой донных отложений 65–70 см)

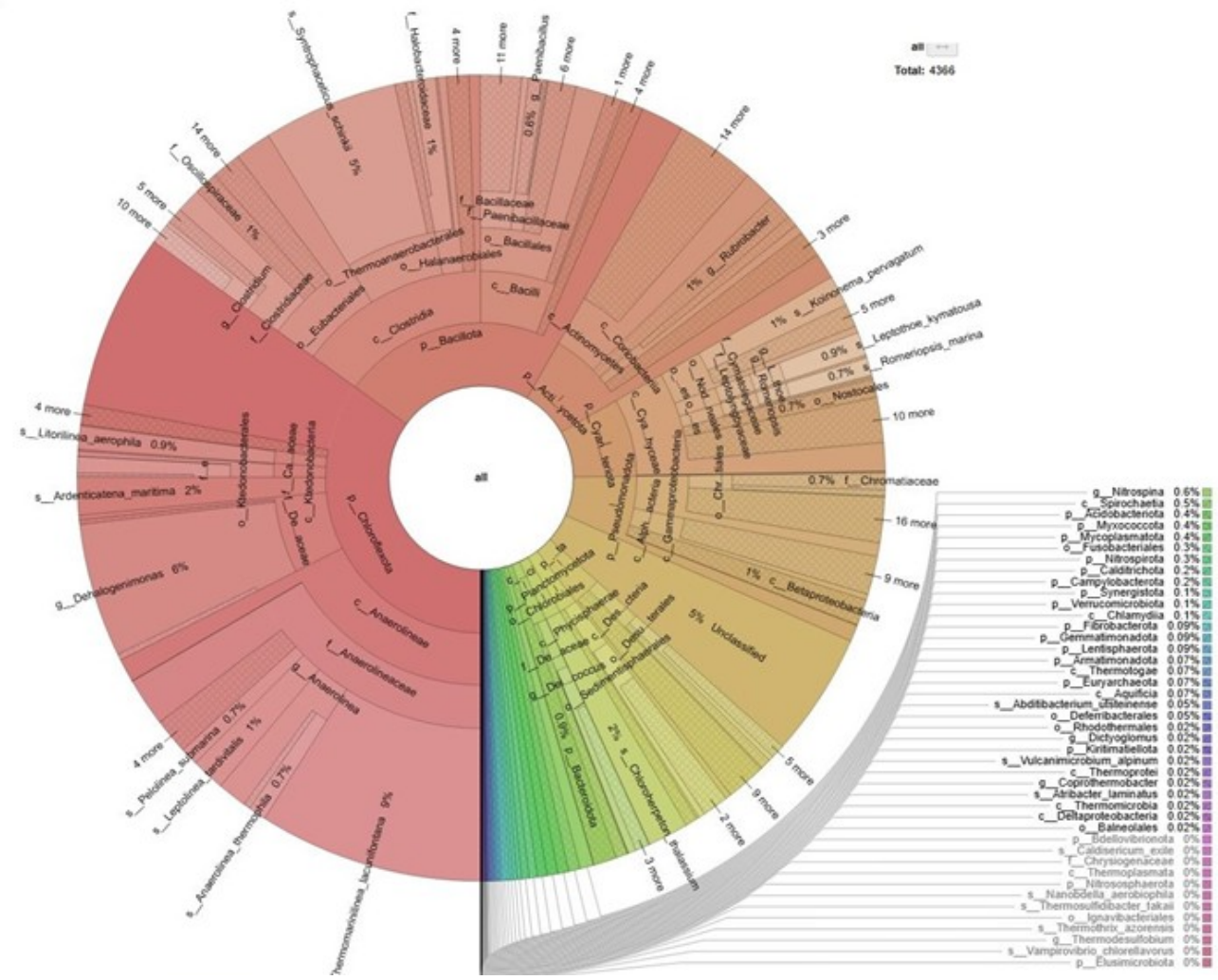

Fig. S1d. The Black Sea bacterial communities represented by dominant OTUs at different levels from samples of bottom sediments; the sample bar5 (st. 1, depth of 2,030 m, layer of bottom sediments of 20–25 cm)

Рис. S1d. Бактериальные сообщества Чёрного моря, представленные доминирующими OTU на разных уровнях в пробах донных отложений; проба bar5 (ст. 1, глубина 2030 м, слой донных отложений 20–25 см)

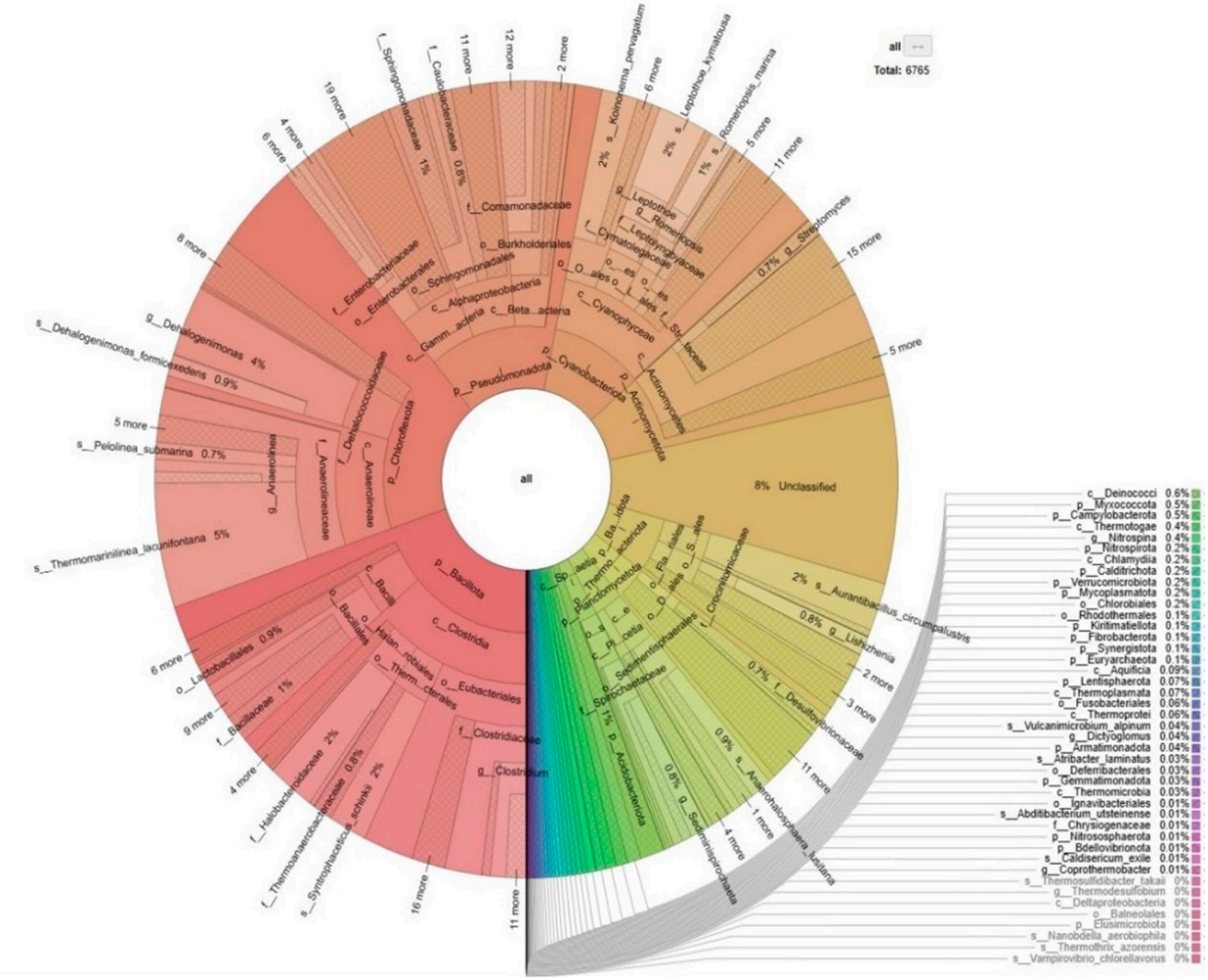

Fig. S1e. The Black Sea bacterial communities represented by dominant OTUs at different levels from samples of bottom sediments; the sample bar6 (st. 1, depth of 2,030 m, layer of bottom sediments of 40–45 cm)

Рис. S1e. Бактериальные сообщества Чёрного моря, представленные доминирующими OTU на разных уровнях в пробах донных отложений; проба bar6 (ст. 1, глубина 2030 м, слой донных отложений 40–45 см)

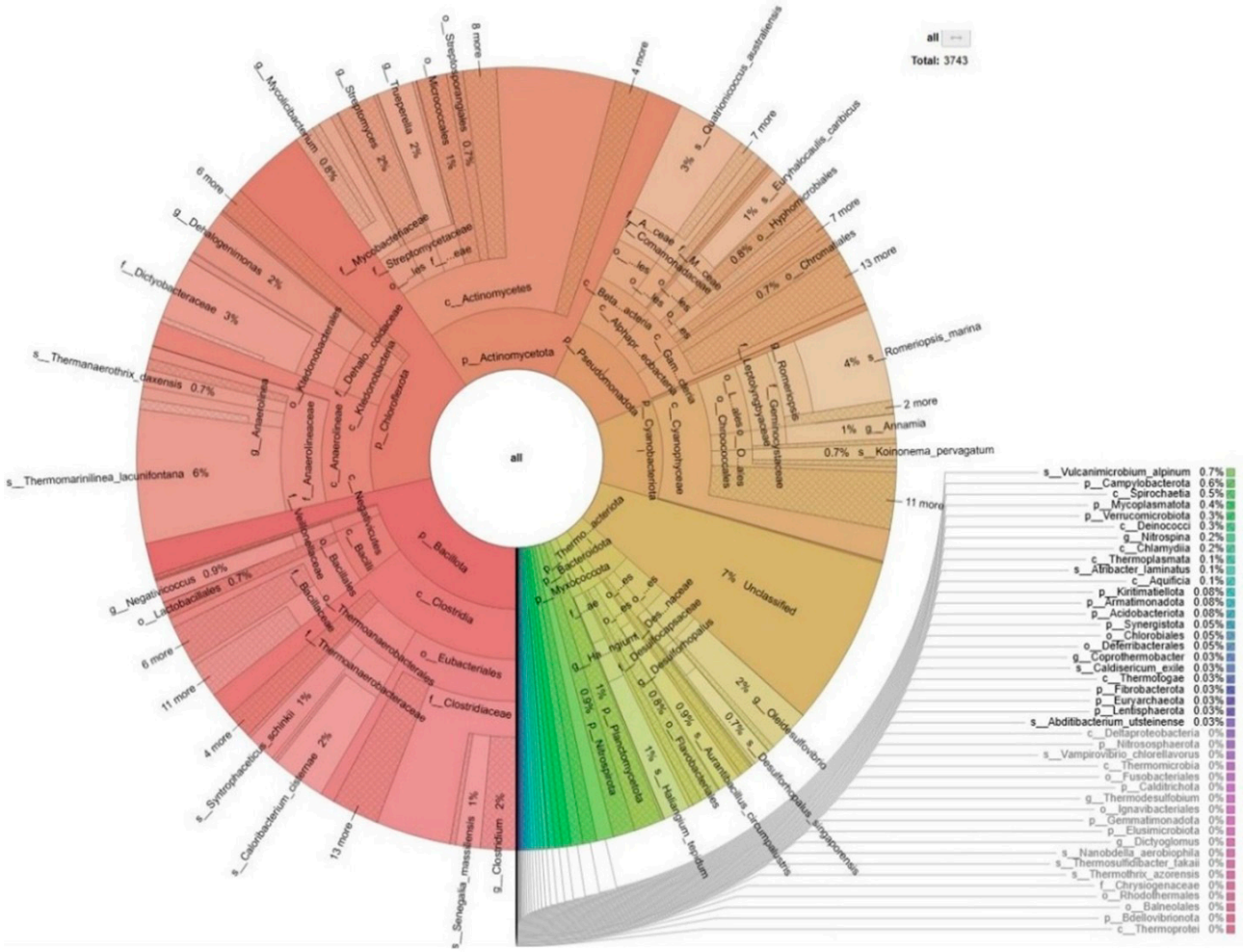

Fig. S1f. The Black Sea bacterial communities represented by dominant OTUs at different levels from samples of bottom sediments; the sample bar7 (st. 1, depth of 2,030 m, layer of bottom sediments of 70–75 cm)

Рис. S1f. Бактериальные сообщества Чёрного моря, представленные доминирующими OTU на разных уровнях в пробах донных отложений; проба bar7 (ст. 1, глубина 2030 м, слой донных отложений 70–75 см)